# ATTACHMENTS:

2) **Computer readable copy of corrected Sequence Listing**

# ATTACHMENTS:

3) **Mark-up of Sequence Listing as originally filed**

SEQUENCE LISTING

VERSION SHOWING CORRECTIONS

<110> Sumitomo Chemical Co., Ltd

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

<130>

<140>
<141>

<160> 27

<170> PatentIn Ver. 2.1

<210> 1
<211> 325
<212> PRT
<213> Penicillium citrinum

<400> 1

Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
1 5 10 15

Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

Lys Asn Leu Ser Ala
325

<210> 2
<211> 978
<212> DNA
<213> Penicillium citrinum

<220>
<221> CDS
<222> (1)..(978)

<400> 2

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Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 1               5                  10                  15

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc   96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
            20                  25                  30

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac  144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
        35                  40                  45

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt  192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
    50                  55                  60

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc  240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65                  70                  75                  80

tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg  288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
                85                  90                  95

tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg  336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
            100                 105                 110
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Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
100 105 110

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
115 120 125

Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
130 135 140

Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
145 150 155 160

Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
165 170 175

Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
180 185 190

Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
195 200 205

Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
210 215 220

Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
225 230 235 240

Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
245 250 255

Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
260 265 270

Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
275 280 285

Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
290 295 300

Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
305 310 315 320

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ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag   384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
        115                 120                 125

ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc   432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
    130                 135                 140

gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat   480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
145                 150                 155                 160

cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt   528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
                165                 170                 175

gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc   576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
            180                 185                 190

gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc   624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
        195                 200                 205

tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac   672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
    210                 215                 220

cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac   720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
225                 230                 235                 240

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc   768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
                245                 250                 255

tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc   816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
            260                 265                 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac   864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
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275 280 285

ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
290 295 300

aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
305 310 315 320

aag aac ctg tct gcg tga 978
Lys Asn Leu Ser Ala
325

<210> 3
<211> 17
<212> PRT
<213> Penicillium citrinum

<400> 3
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1 5 10 15

Pro

<210> 4
<211> 10
<212> PRT
<213> Penicillium citrinum

<400> 4
Ile Pro Gly Val Phe Gly Thr Phe Ala Ser
1 5 10

<210> 5
<211> 17
<212> PRT
<213> Penicillium citrinum

<400> 5
Ser Ile Glu Leu Ser Asp Ala Asp Phe Glu Ala Ile Asn Ala Val Ala
1 5 10 15

Lys

<210> 6
<211> 14
<212> PRT
<213> Penicillium citrinum

<400> 6
Met Ile Gly Val Ala Asn Tyr Thr Ile Ala Asp Leu Glu Lys
1 5 10

<210> 7
<211> 14
<212> PRT
<213> Penicillium citrinum

<400> 7
Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg
1 5 10

<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

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<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 9
tangcnacng gcataatatt 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 10
tangcnacng gcataatgtt 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

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tangcnacng gcatgatatt 20

<210> 12
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 12
tangcnacng gcatgatgtt 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 13
tangcnacng gcattatatt 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 14
tangcnacng gcattatgtt 20

<210> 15
<211> 697
<212> DNA
<213> Escherichia coli

<400> 15

cgctctaaaa ctantggatc ccccgggctg caggaattcg gcggcggcgg atccaacgga 60
aanactttca cactgagcaa cggcgtcaaa attcctggcg tcggctttgg tacctncgct 120
agtgaaggtt ccaagggcga aacctatnct gctgtcacca ctgccctgaa aaccggttac 180
cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtntccgt 240
gacttcctga aggaaaaccc ctcggtgaag cgtgaggaca tcttcgtctg caccaaggtg 300
tggaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagcgt 360
cttggacttg actacgttga tatgttcctc gttcactggc ccattgctgc cgaaaaaaat 420
ggccagggtg agcccaaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc 480
gaaancccna ncccacctgg cgcgctatgg aaaaaatttn tgangatccc aaggccaggt 540
ccattggtgt ttccaattgg accattgccg accttgagaa gatgtccaag ttngccaagg 600
tnatgcctca cgccaaccag atcgagattc accccttcct gcccaacgag gagctggtgc 660
agtactgctt ttccaagaac antatgcccg tagcgta 697

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed oligonucleotide primer for PCR

<400> 16
ggaggtggtt ccacaccttg g 21

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed oligonucleotide primer for PCR

<400> 17
caaccagatc gagattcacc 20

<210> 18
<211> 331

<212> DNA
<213> Escherichia coli

<400> 18
cgctctaaaa ctantggatc ccccgggctg caggaattcg gcggccgcgg atccttcatc 60
cccatcatgt ctaacggaaa gactttcaca ttgagcaacg gcgtcaagat tcctggcgtc 120
ggctttggta ccttcgctag tgaaggttcc aagggcgaga cctatactgc tgtcaccact 180
gcccctgaaga ccggttaccg tcacttggac tgtgcctggt actacctgaa cgagggtgag 240
gttggtgagg gtatccgtga cttcctgaag gagaaccccc cggtgaagcg tgaggacatc 300
ttcgtctgca ccaaggtgtg gaaccacctc c 331

<210> 19
<211> 743
<212> DNA
<213> Escherichia coli

<400> 19
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cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcggcaacac 180
ccttgctcag gttcttattg cctggggtct gcgccgtggc tacgtcgttc tccccaagag 240
ctccaacccc aagcgcattg agtccaactt caagagcatt gagctctccg atgccgactt 300
tgaagccatc aatgccgttg ccaagggtcg tcacttccgt ttcgtcaaca tgaaggatac 360
tttcggatat gatgtctggc ccgaggagac cgccaagaac ctgtctgcgt gaatctctac 420
gaaattataa aatnacaccn acnaaaancc aaagcganag gatgatnccc aaaantttg 480
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tctccaaaaa aaaaaaaaaa aaaaacggtc cgcggccgct ccnnggggg gcccggttcc 600
caattcnccc cttatnattg aattcttttt taanggggnc aaattccncc nnatttccnt 660
cnanattggn nggccgcctc caaactttcn tcntnaaagg gncccaattc ccccccnatt 720
aantggantt cctnttacc ttt 743

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed
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<400> 20
ccaaggtgtg gaaccacctc c 21

<210> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 21
ccagaggaga gtaggccacg g 21

<210> 22
<211> 417
<212> DNA
<213> Escherichia coli

<400> 22
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agaagaatgg ccagggtgag cccaagattg gccctgacgg caaatacgtc attctcaagg 180
acctgaccga gaaccccgag cccacatggc gcgctatgga gaagatttat gaggatcgca 240
aggccaggtc cattggtgtc tccaactgga ccattgccga ccttgagaag atgtccaagt 300
tcgccaaggt catgcctcac gccaaccaga tcgagattca ccccttcctg cccaacgagg 360
agctggtgca gtactgcttc tccaagaaca ttatgcccgt ggcctactct cctctgg 417

<210> 23
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 23

gccatggcta tgtctaacgg aaagact 27

<210> 24
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 24
cggatccgtt ataatttcgt agagattca 29

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 25
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<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 26
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<210> 27
<211> 786
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(786)

<400> 27

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 1               5                  10                  15

acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct   96
Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
            20                  25                  30

aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gaa gct aac agc gtt   144
Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
        35                  40                  45

tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt   192
Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
    50                  55                  60

gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att   240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
65                  70                  75                  80

aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa   288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
                85                  90                  95

aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc   336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
            100                 105                 110

att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att   384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
        115                 120                 125
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```
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg  432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
    130                 135                 140

agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca  480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145                 150                 155                 160

agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac  528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
                165                 170                 175

gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat  576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
            180                 185                 190

aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat  624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
        195                 200                 205

gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att  672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
    210                 215                 220

gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca  720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
225                 230                 235                 240

ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc  768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
                245                 250                 255

caa gca gga cgc gga taa                                         786
Gln Ala Gly Arg Gly
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<210> 28
<211> 996
<212> DNA
<213> Penicillium citrinum

<220>
<221> CDS
<222> (1)..(978)

<400> 28

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atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct   48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 1               5                  10                  15

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc   96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
            20                  25                  30

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac  144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
        35                  40                  45

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt  192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
    50                  55                  60

gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc  240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65                  70                  75                  80

tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg  288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
                85                  90                  95

tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg  336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
            100                 105                 110

ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag  384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
        115                 120                 125

ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc  432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
    130                 135                 140

gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat  480
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```
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
145                 150                 155                 160

cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt  528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
                165                 170                 175

gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc  576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
            180                 185                 190

gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc  624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
        195                 200                 205

tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac  672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
    210                 215                 220

cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac  720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
225                 230                 235                 240

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc  768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
                245                 250                 255

tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc  816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
            260                 265                 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac  864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
        275                 280                 285

ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc  912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
    290                 295                 300

aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc  960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
305                 310                 315                 320
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aag aac ctg tct gcg tga atctctacga aattataa 996
Lys Asn Leu Ser Ala
325

<210> 29
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence Designed oligonucleotide primer for PCR

<400> 29
cggatccgtt cacgcagaca ggttcttgg 29

<210> 30
<211> 978
<212> DNA
<213> Penicillium citrinum

<220>
<221> CDS
<222> (1)..(978)

<400> 30
atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
1 5 10 15

ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
20 25 30

tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
35 40 45

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

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gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc   240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65                  70                  75                  80

tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg   288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
                 85                  90                  95

tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg   336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
            100                 105                 110

ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag   384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
        115                 120                 125

ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc   432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
    130                 135                 140

gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat   480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
145                 150                 155                 160

cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt   528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
                165                 170                 175

gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc   576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
            180                 185                 190

gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc   624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
        195                 200                 205

tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac   672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
    210                 215                 220

cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac   720
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Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
225 230 235 240

gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc 768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
245 250 255

tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
260 265 270

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
275 280 285

ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
290 295 300

aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
305 310 315 320

aag aac ctg tct gcg tga 978
Lys Asn Leu Ser Ala
325

<210> 31
<211> 27
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence Designed oligonucleotide primer for PCR

<400> 31
gccatggcta tgtataaaga tttagaa 27

<210> 32
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
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<223> Description of Artificial Sequence Designed oligonucleotide primer for PCR

<400> 33
cggatccgag cgcccaatac gcaaaccg 28

<210> 34
<211> 385
<212> PRT
<213> Corynebacterium sp.

<400> 34

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Met | Lys | Ala | Ile | Gln | Tyr | Thr | Arg | Ile | Gly | Ala | Glu | Pro | Glu | Leu | Thr |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Glu | Ile | Pro | Lys | Pro | Glu | Pro | Gly | Pro | Gly | Glu | Val | Leu | Leu | Glu | Val |
| | | | 20 | | | | 25 | | | | | 30 | | | |
| Thr | Ala | Ala | Gly | Val | Cys | His | Ser | Asp | Asp | Phe | Ile | Met | Ser | Leu | Pro |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Glu | Glu | Gln | Tyr | Thr | Tyr | Gly | Leu | Pro | Leu | Thr | Leu | Gly | His | Glu | Gly |
| | 50 | | | | 55 | | | | | 60 | | | | | |

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
180 185 190

His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp
305 310 315 320

Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
325 330 335

Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
340 345 350

Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
355 360 365

Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

Arg
385

<210> 35
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Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144

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Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
          35                  40                  45

gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc  192
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
     50                  55                  60

gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc  240
Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 65                  70                  75                  80

gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg  288
Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
                 85                  90                  95

cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc  336
His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
            100                 105                 110

gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc  384
Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
        115                 120                 125

atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac  432
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
    130                 135                 140

ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac  480
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145                 150                 155                 160

gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt  528
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
                165                 170                 175

gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc  576
Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
            180                 185                 190

cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag  624
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
        195                 200                 205
```

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ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac   672
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
    210                 215                 220

aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc   720
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
225                 230                 235                 240

gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg   768
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
                245                 250                 255

atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg   816
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
            260                 265                 270

gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag   864
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
        275                 280                 285

gct tcg gtg aca gtt ccg tat tgg ggt gcc cgc aac gag ttg atc gaa   912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
    290                 295                 300

ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac   960
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp
305                 310                 315                 320

ctt cag tct cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg  1008
Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
                325                 330                 335

aac gct cag cgg ccg tgc ggt tgt ggt ccc tgg tct gta gta ccg aca  1056
Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
            340                 345                 350

gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccg aat tcg att  1104
Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
        355                 360                 365

cgg ccg ggc atc agt gtc aga aat tcg gtg tgc gct agc tgc acg cct  1152
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Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
370 375 380

cga tga 1158
Arg
385